Protein and amino acids recovery from brewer's spent grains by different pretreatment technologies

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Protein and amino acids recovery from brewer's spent grains by different pretreatment technologies

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Protein has extensive use as ingredient in the food and feed industries. With the growing population, the global demand for protein in 2030 is expected to exceed the current production capacities. Therefore, finding alternative sources of protein is a topic of great interest nowadays to meet the future demand of this component. Residual biomass and side streams are potentially interesting sources of this ingredient. However, exploitation of these sources for obtaining proteins is still at an early stage. Brewer´s spent grains (BSG) is an agro-industrial residue rich in proteins, which correspond to approximately 18-20% of its composition in a dry weight basis. In the present study, different pretreatment strategies were evaluated with the aim of recovering protein and amino acids from BSG. Protein fractions, including amino acid, were fully recovered using a pretreatment in three sequential steps (aqueous, alkaline and dilute acid). When comparing the three stages, the greatest part of protein (80.7%) was recovered during the alkaline step, followed by the dilute acid step (10.25%). HPLC analysis revealed that the total amount of amino acid recovered by this sequential pretreatment corresponded to 0.5 g/100 g BSG. The amino acids present in BSG were also identified and quantified. Extraction using only one step dilute acid pretreatment (at different acid concentrations) was also assayed but resulted in much lower protein recovery (between 13.0% and 28.6%) and higher solubilization of the hemicellulose fraction, which is not convenient in a biorefinery perspective. The results also revealed that defatting BSG previous the extraction is not necessary to improve the protein recovery efficiency.

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Ethanol tolerance investigated using data integration from 'omics', systems biology and cell biology

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Bioethanol has been shown as an excellent alternative energy source of fossil fuels. The yeast *Saccharomyces cerevisiae* is the most used microorganism for bioethanol production. However, the ethanol concentration is one of the limiting factors for ethanol production because, at high concentrations, this compound disturbs cells and reduces the productivity. Despite many studies on this topic, the integrated view of 'omics', systems biology and cell biology approaches are far from to be explored. Thus, the selection of target genes to improve the ethanol tolerance for genetic engineering is not trivial. The upper limit to tolerate ethanol stress along 1h was defined for six different haploid strains and unsupervised learning was used to cluster each one as highest tolerant (HT) and lowest tolerant (LT). Differential expression analysis using RNA-Seq for those treatments and controls were performed. The results showed that genes involved in mitochondrial metabolism (matrix, membranes and oxidative stress), peroxisome, nucleoplasm, endoplasmic reticulum lumen, nucleoplasm, protein digestion and homeostasis are deregulated in HT strains; while DNA repair, vesicle-mediated transport, transcription regulation, replication and apoptosis are deregulated in LTs. Proteomics by mass-spectrometry reported that alcohol